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G protein-coupled lymphocyte-specifi G protein-coupled G protein-coupled G protein-coupled G protein-coupled couropeptide Y-pep chemokine (C-C) reneuropeptide Y-pep chemokine (C-C) reneuropeptide Y-pep chemokine (C-C) refusin (LESTRA) - c
                                         interleukin-8 rece
chemokine (C-C) re
interleukin-8 rece
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                                                                                                                MIP-1 alpha recept interferon-inducib chemokine (C-C) re chemokine (C-C) re G protein-coupled interleukin-8 rece
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interleukin-8 rece
MIP-1 alpha recept
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F;160-180/Domain: t
F;212-233/Domain: t
F;250-271/Domain: t
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A; Residues: 1-369 <ZAB>
A; Cross-references: EMBL: Z79784;
C; Comment: This protein belongs t
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Biochem. Biophys. Res. Commun. 227, 846-853, 1996
A;Title: Molecular cloning and RNA expression of two new human
A;Reference number: JC5067; MUID:97040707; PMID:8886020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G protein-coupled receptor CKR-L3 - hun C;Species: Homo sapiens (man) C;Date: 31-Jan-1997 #sequence_revision C;Accession: JC5068
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QGSDVCEPKYQTVSEPIRWKLLMLGLELLFGFFIPLMFMIFCYTFIVKTLVQAQNSKRHK
                                                                                                                                                                          AFYKKARSMIDVYLLNMAIADILEVLILDEWAVSHATGAWVESNATCKLLKGIVAINENC
AIRVIIAVVLVFLACQIPHNMVLLVTAANLGKMNRSCQSE----KLIGYTKTVTEVLAFL
                                                                                                                                 SLKIIFLVMAVFLLTQMPFNLM------KFIRSTHWEYYAMTSFHYTIMVTEAIAYL
                                                                                                                   GMLLLTCISMDRYIAIVQATKSFRLRSRTLPRSKIICLVVWGLSVIISSSTFVFNQKYNT
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JQ4304
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Pred. No. 1.
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angiotensin II rec
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interleukin-8 rece
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Result No.

Score

Query Match

Length

DB

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Description

619 608.5 608.5 588.5 568

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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495.5 494 491.5

524.5
521.5
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507.5
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JW0621 A4577 138450 C22443 C600048 A48177 A45177 A45177 A4517160 JW160041 A53752 JW160049 JW1

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 s

summaries

Database

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Minimum DB Maximum DB

seq

length: length:

2000000000

al number rched:

of hits satisfying chosen parameters:

Title: Perfect score:

US-09-940-063-2 1794

1 MAEHDYHEDYGFSSFNDSSQ..

......DNSKTFSASHNVEATSMFQL

Scoring table:

BLOSUM62 Gapop 10.0 ,

Gapext 0

283224 seqs,

96134422 residues

OM protein -

protein search, using sw model

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen

July 15, 2003, 07:15:55; Search time 41 Seconds (without alignments) 801.902 Million cell updates/sec

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RESULT 3
A55735
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Genomics 23, 643-650, 1994

A;Title: Cloning of human and mouse EBI1, a lymphoid-specific G-protein-coupled recepto:
A:Reference number: A55735; MUID:95154835; PMID:7851893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N;Alternate names: Burkitt's lymphoma receptor 2; E
C;Species: Homo sapiens (man)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995
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A;Description: The expression of the chemokine receptor BLR2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: S52443
A; Accession: S52443
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A; Residues: 21-378 <BUR>
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//Alternate names: Burkitt's lymphoma receptor 2; Epstein-Barr virus induced
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;Schweickart, V.L.; Raport, C.J.; Godiska,
enomics 23, 643–650, 1994
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Residues: 1-378 <SCH>
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                                                                                               PYLGVSHQWKSSEDNSKTFSASHNVEATSMF 340
                                                                 SQEQL-RQWSSCR-HIRRSSMSVEAETTTTF 376
                                                                                                                                                                                                                            LGFFLPLLTMIVCYSVIIKTLLHAGGFQKHRSLKIIFLVMAVFLLTQMPFN-----LM
                                                                                                                                  NFNITSSTCELSKOLNIAYD--VTYSLACVRCCVNPFLYAFIGVKFRNDLFKLFKDLGCL
                                                                                                                                                      KF-IRSTHWEYYAMTSFHYTIMVTEAIAYLRACLNPVLYAFVSLKFRKNFWKLVKDIGCL 309
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Pred. No. 9.1e-42;
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                                                                                              Similarity
         KDVRNEKAWELPIMYSIICEVGLLGNGLVVLTYIYEKRLKTMTDTYLLNLAVADILELLT 110
                                       QDELQESKVELPCMYLVVFVCGLYGNSLVLVISIFYHKLQSLTDVFLVNLPLADLVFVCT 83
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RESULT 4
A45680
G protein-coupled peptide receptor EBC; Species: Homo sapiens (man)
C; Date: 21-Sep-1993 #sequence_revisic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:L31580; NID:g468340; C;Superfamily: vertebrate rhodopsin C;Keywords: G protein-coupled receptor
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                                              A;Cross-references: GB:L08176; NID:g183484; PID:g183485
A;Experimental source: B-lymphocytes
A;Note: sequence extracted from NCBI backbone (NCBIN:127094,
                                                                                                                         A; Molecule type: nucleic acid
A; Residues: 1-378 <BIR>
                                                                                                                                                                                              J. Virol. 67, 2209-2220, 1993
A;Title: Epstein-Barr virus-induced genes:
A;Reference number: A45680; MUID:93188173;
A;Accession: A45680
                                                                                                                                                                                                                                                                 R;Birkenbach, M.; Josefse
J. Virol. 67, 2209-2220,
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Superfamily: vertebrate rhodopsin Reywords: G protein-coupled recept
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9-2220, 1993
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Pred. No. 9.1e-42;
4; Mismatches 108;
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32.8%;

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Mismatches

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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CKRB_BOVIN
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CKR2_MOUSE
IL8B_RABIT
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                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                           Loetscher M., Amara A., Oberlin E., Brass N., Legler D.F.,
Loetscher P., D'Apuzzo M., Meese E.U., Rousset D., Virelizier
Baggiolini M., Arenzana-Seisdedos F., Moser B.;
"TYMSTR. a putative chemokine receptor selectively expressed i
activated T cells, exhibits HIV-1 coreceptor function.";
Curr. Biol. 7:652-660(1997).
-I- FUNCTION: RECEPTOR FOR THE C-x-C CHEMOKINE CXCL16. USED AS
CORECEPTOR BY SIVS AND BY STRAIMS OF HIV-2 AND M-TROPIC HI
-I- SUBCELLULAR LOCATION: Integral membrane protein.
-I- TISSUE SPECIFICITY: EXPRESSED IN LYMPHOID TISSUES AND ACTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C-X-C chemokine receptor type 6 (CXC-R6) (CXCR-6) (G receptor bonzo) (G protein-coupled receptor STRL33). CXCR6 OR BONZO OR STRL33 OR TYMSTR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "STRL33, A novel chemokine receptor-like protein, functions as a fusion cofactor for both macrophage-tropic and T cell line-tropic HIV-1.";
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
EMBL; AF007545; AAB64221.1;
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Farber J.M.;
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Best Local
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                                    15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
C-X-C chemokine receptor type 6 (CXC-R6) (CXC
Macaca nemestrina (Pig-tailed macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Kammalia; Eutheria; Primates; Catarrhini; Cercopithe
                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
DISULFID
                         CXCR6
                                receptor
                                                                      019024;
                                                                              CCR6_MACNE
                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1. PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1. G-protein coupled receptor; Transmembrane;
                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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PRINTS; PR00237; GPCRRHODOPSN
                                                                                                                                                                                                                                                                                                                                                       VARIANT
                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
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                       OR BONZO
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U73531; AAB61457.
Y13248; CAA73698.
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                                                                                                                                                                                                                                                                                                                 Similarity
                               bonzo).
                                                                                                                                                KLQSLTDVFLVNLPLADLVFVCTLPFWAYAGIHEWVFGQVMCKSLLGIYTINFYTSMLIL
                                                                                                                                                                                                                                                                                  MAEHDYHEDYGFSSFNDSSQEEHQDFLQFSKVFLPCMYLVVFVCGLVGNSLVLVISIFYH
                                                                                                                   KLVKDIGCLPYLGVSHQWKSSEDNSKTFSASHNVEATSMFQL
                                                                                                                          KLVKDIGCLPYLGVSHQWKSSEDNSKTFSASHNVEATSMFQL
                                                                                                                                                                                                             TCITVDRFIVVVKATKAYNQQAKRMTWGKVTSLLIWVISLLVSLPQIIYGNVFNLDKLIC
                                                                                                                                                                                                                     TCITVDRFIVVVKATKAYNQQAKRWTWGKVTSLLIWVISLLVSLPQIIYGNVFNLDKLIC
                                                                                                                                                                                                                                           KLQSLTDVFLVNLPLADLVFVCTLPFWAYAGIHEWVFGQVMCKSLLGIYTINFYTSMLIL
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                                                                              STANDARD;
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4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

7 (POTENTIAL).
                                                                                                                                                                                                                                                                                                        0;
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CYTOPLASMIC (P
BY SIMILARITY.
N-LINKED (GLCN
D -> A (IN STR
                                                                                                                                                                                                                                                                                                        Score 1794; DB 1;
Pred. No. 8.1e-95;
; Mismatches 0;
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9FBC025556D1082E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL)
3 (POTENTIAL).
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2 (POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ransmembrane; Glycoprotein; EXTRACELLULAR (POTENTIAL).
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IN STRL33.3).
                                       (CXCR-6)
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 ertebrata; Euteleostomi;
Cercopithecidae;
                                       G
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                                       protein-coupled
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cercopithecinae;
NCBI_TaxID=9545;
[1]
                                                                                                                                                                                                                     DISULFID
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                                                                                                                                                                       al Similarity
327; Conserv
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in coupled
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PRINTS; PR00237; GPCRRHODOPSN PROSITE; PS00237; G_PROTEIN_RI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Deng H.K., Unutmaz D., Kewalramani V.N., Littme "Expression cloning of new receptors used by si immunodeficiency viruses.";
Nature 388:296-300(1997).
-I- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE CORECEPTOR BY SIYS AND BY STRAINS OF HIV-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF007858; AAB64224.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED
                                                                                                                GYHDEAISTVVLATQMTLGFELPLLTMIVCYSVIIKTLLHAGGFQKHRSLKIIFLVMAVF
                                                                                                                                                                                   TCITVDRFIVVVKATKAYNQQAKRMTWGKVTSLLIWVISLLVSLPQIIYGNVFNLDKLIC
                                                                                                                                                                                                                                MAEHDYHEDYGFSSFNDSSQEEHQDFLQFSKVFLPCMYLVVFVCGLVGNSLVLVISIFYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              non-profit instituend this statement
KLVKDIGCLPYLGVSHQWKSSEDNSKTFSASHNVEATSMFQL
                                                LLTQMPFNLMKFIRSTHWEYYAMTSFHYTIMVTEAIAYLRACLNPVLYAFVSLKFRKNFW
                                                                                                                                                                                                                                                                                              MAEHDYHEDYGLNSFNDSSQEEHQDFLQFRKVFLPCMYLVVFVCGLVGNSLVLVISIFYH
                                                                                              GYHDKEISTVVLATQMTLGFFLPLLAMIVCYSVIIKTLLHAGGFQKHRSLKIIFLVMAVF
                                                                                                                                                                  TCITVDRFIVVVKATKAYNQQAKRMTWGKVICLLIWVISLLVSLPQIIYGNVFNLDKLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS00237; G_PROTEIN_RECEP_F1_1; PS50262; G_PROTEIN_RECEP_F1_2;
                                LLTQTPFNLVKLIRSTHWEYYAMTSFHYTIIVTEAIAYLRACLNPVLYAFVSLKFRKNFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR000276; GPCR_Rhodpsn
                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 license
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CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
N-LINKED (GLCNAC...) (PC
W; 55F9F68CB62D2DF5 CRC64;
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4 (POTENTIAL).

5 (POTENTIAL).

5 (POTENTIAL).

6 (POTENTIAL).

6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

7 (POTENTIAL).
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EXTRACELLULAR (
3 (POTENTIAL)
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CYTOPLASMIC (POTENTIAL)
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EXTRACELLULAR
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                                                                                                                                                                                                                                                                                                                                                             Score 1730; DB 1;
Pred. No. 3.2e-91;
7; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (See http://www.isb-sib.ch/announce/
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d by simian an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
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AND M-TROPIC
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342
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HIV-1.
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300

240

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RESULT 3
CCR6_CERAE
ID CCR6_C
AC 018983
DT 15-JUL
DT 15-JUL
DT 15-JUN
DT C-X-C
DE recept
GN CXCR6
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OC Mammal
OC Cercop
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15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
C-X-C chemokine receptor type 6 (CXC-R6) (CXCR-6)
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DOMAIN
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TRANSMEM
                                                                                                                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                     SEQUENCE
                                                                                                               CARBOHYD
                                                                                                                        DISULFID
                                                                                                                                               TRANSMEM
                                                                                                                                                           DOMAIN
                                                                                                                                                                    TRANSMEM
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Deng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Cercopith
                                                                                                                                    DOMAIN
                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00237; GPCRRHODOPSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 388:296-300(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Deng H.K., Unutmaz D., Kewalramani V.N., "Expression cloning of new receptors use immunodeficiency viruses.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97373958; PubMed=9230441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE CXCL16. USED CORECEPTOR BY SIVS AND BY STRAINS OF HIV-2 AND M-TROPIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CERAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301
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              _
                                  \vdash
                                                                   Similarity
                                                                                                                                                                                                                                                                                   PS00237; G_PROTEIN_RECEP_F1_1; 1.
PS50262; G_PROTEIN_RECEP_F1_2; 1.
n coupled receptor; Transmembrane; Glycoprotein.
1 32 EXTRACELLULAR (POTENTIAL).
            bonzo).
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                                                        Conservative
                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                       39226
                                                                  95.7%;
95.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Integral membrane
                                                                                                   MW;
                                                     9;
                                                     Score 1717; Db 1,
Pred. No. 1.7e-90;
Pred. No. 1.7e-90;
                                                                                                                       7 (POTENTIAL).
CYTOPLASMIC (F
BY SIMILARITY.
                                                                                                                                                                   EXTRACELLULAR (
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (F
                                                                                                              N-LINKED
                                                                                                                                                                                                                       3 (POTENTIAL)
CYTOPLASMIC (
                                                                                                                                                                                                                                            EXTRACELLULAR
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                                                                                                   6CBFE389C6E5919E CRC64;
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                                                                                                              (GLCNAC
                                                                                                                                                                                                                                                                (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Littman D.
1 by simian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B
                                                                                                                                  (POTENTIAL)
                                                                                                                                                                            (POTENTIAL).
                                                                                                                                                                                                                      (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cercopithecidae;
                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                  (POTENTIAL)
                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein
                                                                          Length 342
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                                                        Indels
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                                                                                                             (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human
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HIV-1.
                                                        0;
                                                        Gaps
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CCR6_MACMU
   В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCR6_MACMU
Q9XT45;
16-OCT-2001
  DOMAIN
TRANSMEM
                                  TRANSMEM
DOMAIN
                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor bonzo) (G protein-coupl CXCR6 OR BONZO OR STRL33.
Macaca mulatta (Rhesus macaque).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
C-X-C chemokine receptor type 6 (CXC-R6) (CXCR-6)
                                                                                                                                                       EMBL; AF124380; AAD31419.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                 This
                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Ve Mammalia; Eutheria; Primates; Catarrhini; Cercopithecinae; Macaca.
                                                                                                           G-protein
                                                                                                                                                                                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                     use by non-profit institutions a modified and this statement is not
                                                                                                                                                                                                                                                                                                                                  receptors.
                        TRANSMEM
                                                       DOMAIN
                                                                  TRANSMEM
                                                                            DOMAIN
                                                                                       TRANSMEM
                                                                                                  DOMAIN
                                                                                                                                              PRINTS;
                                                                                                                                                                                                                                          the European Bioinformatics Institute.
                                                                                                                                                                                                                                                     between the
                                                                                                                                                                                                                                                                                                        AIDS Res. Hum. Retroviruses 17:981-986(2001).
-I- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE CXCL16. USED CORECEPTOR BY SIVE AND BY STRAINS OF HIV-2 AND M-TROPIC
                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21354176; PubMed=11461684;
Margulies B.J., Hauer D.A., Clements J.E.
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 15-JUN-2002 (Rel.
                                                                                                                                                                                                                                                                                                                                                        'Identification
                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301
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                                                                                                                        PS00237;
PS50262;
                                                                                                                                            PR00237; GPCRRHODOPSN
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G_PROTEIN_RECEP_F1_2;
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EXTRACELLULAR

1 (POTENTIAL).

CYTOPLASMIC (POCENTIAL).

2 (POTENTIAL).

EXTRACELLULAR
3 (POTENTIAL).

CYTOPLASMIC (PC
4 (POTENTIAL).

EXTRACELLULAR
4 (POTENTIAL).
                                                                                                           Transmembrane;
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                                  (POTENTIAL).
                                                                           (POTENTIAL).
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                                                                                                Glycoprotein (POTENTIAL).
                                                     (POTENTIAL)
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Euteleostomi;

chemokine

AS A HIV-1.

.isb-sib and

.ch/announce,

for

a collaboration -MBL outstation -

outstation

9

protein-coupled

SQUETT

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RESULT 5
CKR6_HUMAN
ID CKR6_H
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Best Local S
Matches 325
Biochem.
[,4]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P51684; 092846; P78553;
01-0CT-1996 (Rel. 34, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
C-C chemokine receptor type 6 (C-C CKR-6) (CC-CKR-6) (CCR-6) (LARC receptor) (GPR-CY4) (GPRCY4) (Chemokine receptor-like 3) (CKR-L3)
                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND FUNCTION.
MEDLINE-97313465; PubMed-9169459;
Baba M., Imai T., Nishimura M., Kakiza
Nomiyama H., Yoshie O.;
"Identification of CCR6, the specific
lymphocyte-directed CC chemokine LARC.
J. Biol. Chem. 272:14893-14898(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
DISULFID
SEQUENCE
                                 Zaballos A., Varona R., Gutierrez J., "Molecular cloning and RNA expression receptor-like genes.";
                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM DOMAIN
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TRANSMEM
                                                                                       SEQUENCE FROM N.A. MEDLINE=97040707; PubMed=8886020;
                                                                                                                                               Lautens L.
Submitted
                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCR6 OR CMKBR6 OR STRL22 OR GPR29 OR CKRL3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CKR6_HUMAN
                                                                                                                                                                   Lautens
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                                                                                                                                           E FROM N.A.
L.L., Modi W.,
ed (APR-1996) tc
                 Biophys.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGYHDEEISTVVLATQMTLGFFLPLLAMIVCYSVIIKTLLHAGGFQKHRSLKIIFLVMAV
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the EMBL/GenBank/DDBJ
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6 (POTENTIAL).
7 (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
BY SIMILARITY.
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Pred. No. 1.1e-89;
9; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Catarrhini; Hominidae
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               227:846-853(1996)
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                                                  Marquez
new human
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FINANCIA CON CONTROL CO
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EMBL; U60000; AAB06949.1;
EMBL; U68030; AAC51124.1;
EMBL; U68032; AAC51125.1;
                                                                                                                                                                                                                                                              entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor 6q27.";
                                                                                  MIM; 601835;
                                                                                                                                                                                                  EMBL; U45984; AAB62714.1; EMBL; Z79784; CAB02144.1;
                                                                                                                                                                                                                                                                                                        modified
InterPro; IPR000020; Anaphylatoxi;
InterPro; IPR004067; CC_chemkine6
InterPro; IPR000276; GPCR_Rhodpsn
Pfam; PF00001; 7tm_1; 1.
                                                                                                                      HSSP; P34996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MCCOy R., Perlmutter Submitted (SEP-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomics 40:175-180(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                             INTRACELLULAR CALCIUM IONS LEVEL.
SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: SPLEEN, LYMPH NODES, APPENDIX, AND FETAL
LYVER. EXPRESSED IN LYMPHOCYTES, T CELLS AND B CELLS BUT NOT IN
NATURAL KILLER CELLS, MONCOTTES, OR GRANULOCYTES.
INDUCTION: BY INTERLEUKIN 2.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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                                                                                                                                                                                                                                                                                                                                            ween the Swiss Institute of Bioinformatics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION:
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                                                                                                 HGNC: 1607;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| 16                | 15     | 14                | 13     | 12                 | 11                 | 10                 | 9                  | 8                  | 7                  | 6                  | u                  | 4                  | ω                 | N                  |                    | Result<br>No.         |
|-------------------|--------|-------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|-----------------------|
| 528               | 529.5  | 530.5             | 551.5  | 554.5              | 584                | 605.5              | 612                | 771                | 783                | 1326               | 1332               | 1690.5             | 1692.5            | 1785               | 1790               | Score                 |
| 29.4              | 29.5   | 29.6              | 30.7   | 30.9               | 32.6               | 33.8               | 34.1               | 43.0               | 43.6               | 73.9               | 74.2               | 94.2               | 94.3              | 99.5               | 99.8               | Query<br>Match Length |
| 346               | 347    | 355               | 350    | 350                | 368                | 367                | 369                | 149                | 150                | 351                | 351                | 343                | 343               | 342                | 342                | Length                |
| 6                 | 6      | 6                 | 11     | 11                 | 13                 | 11                 | 4                  | σ                  | σ                  | 11                 | 11                 | 6                  | σ                 | σ                  | 4                  | DB                    |
| Q9MZM4            | Q9MZN4 | 8ГАМ6О            | Q8QZW9 | Q924I3             | 042444             | Q9R1V0             | 90006              | Q8WNM7             | 8MNM8              | Q9ERH5             | Q9EQ16             | Q9BDS6             | Q9N0Z0            | Q9TV16             | Q9HCA5             | ID                    |
| Q9mzm4 nycticebus | hylo   | Q9myj8 callithrix | -      | Q924i3 mus musculu | O42444 oncorhynchu | Q9rlv0 mus musculu | Q9uqq6 homo sapien | Q8wnm7 pongo pygma | Q8wnm8 gorilla gor | Q9erh5 mus musculu | Q9eq16 mus musculu | Q9bds6 macaca fasc | Q9n0z0 cercocebus | Q9tv16 pan troglod | Q9hca5 homo sapien | Description           |

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| 45        | 44        | 43        | 42     | 41          | 40     | 39           | 38     | 37        | 36     | 35      | 34     | 33          | 32       | 31    | 30                 | 29         | 28     | 27                 | 26     | 25     | 24        | 23     | 22        | 21     | 20         | 19     | 18     | 17                |
|-----------|-----------|-----------|--------|-------------|--------|--------------|--------|-----------|--------|---------|--------|-------------|----------|-------|--------------------|------------|--------|--------------------|--------|--------|-----------|--------|-----------|--------|------------|--------|--------|-------------------|
| 515.5     | 515.5     | 515.5     | 515.5  | 515.5       | 515.5  | 515.5        | 515.5  | 516       | •      |         |        | •           | •        | •     | •                  |            | •      |                    | ٠      |        | ٠         | •      | 524.5     | •      | •          |        | 528    | N                 |
| 28.7      | 28.7      | 8         | 8      | 8           | 8      | 8            | 8      | 8         | ω.     | œ       | ω.     | 8           | 8        | 9.    | 9                  | 9          | 9      | 9.                 | 9      | 9      | 9         | 9      | 29.2      | 9.     | 9          | 9.     | 9.     | 9.                |
| 347       | 347       | 347       | 347    | 347         | 347    | 347          | 347    | 334       | 347    | 347     | 347    | 349         | 347      | 347   | 347                | 352        | 347    | 347                | 347    | 347    | 347       | 347    | 347       | 353    | 347        | 347    | 346    | 346               |
| σ         | 0         | δ         | σ      | σ           | σ      | 0            | σ      | σ         | σ      | 6       | σ      | 11          | Φ        | σ     | σ                  | 4          | σ      | σ                  | 9      | σ      | σ         | 9      | 0         | 13     | Q          | 6      | 6      | ġ                 |
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| presbytis | 5 presbyt | 3 colobus | _      | 0 pygathrix | _      | 2 rhinopithe |        | hylobates | _      | mandril | ש      | 7 rattus no | callimic | w     | Q9mzp7 presbytis s | homo sapie | C,     | Q9mzn1 gorilla gor |        |        | hylobates |        | ateles pa | Ġ      | callicebus |        |        | Q9mzm3 nycticebus |

## ALIGNMENTS

| E HIV-1 infection."; abases. Indels 0; Gaps 0 | Query Match 99.8%; Score 1790; DB 4; IBest Local Similarity 99.7%; Pred. No. 4.9e-141; Matches 341; Conservative 1; Mismatches 0; | J. Exp. med. 185:2015-2023(1997).  [2]  SEQUENCE FROM N.A.  An P., Winkler C., O'Brien S.J.;  An P., Winkler C., O'Brien S.J.;  The Influence of a STRL33 mutant on the cour.  "The Influence of A STRL33 mutant on the cour.  Submitted (OCT-1997) to the EMBL/GenBank/DDBJ  EMBL; AF029759; AAG21918.1;  InterPro; IPR000276; GPCR_Rhodpsn.  PRINTS; PR000237; GPCRRHODOPSN.  PRINTS; PR00237; GPCRRHODOPSN.  PRINTS; PR01568; LYMPHOTACTNR.  PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOPROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.  Receptor.  Receptor.  342 AA; 39279 MW; CE149633D01D20. | RESULT 1  Q9HCA5  ID Q9HCA5  PRELIMINARY; PRT; 342 AA.  C Q9HCA5  PRESULT 16, Created)  DT Q1-MAR-2001 (TrEMBLrel. 16, Created)  DT Q1-MAR-2001 (TrEMBLrel. 121, Last sequence update)  DT Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)  DT Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)  DE Mutant G protein-coupled receptor STRL33.  GN STRL33.  GN STRL33.  CS Homo sapiens (Human).  OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo:  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  OC MCBL_TaxID=9606;  RN [1]  RP SEQUENCE FROM N.A.  RY MEDLINE-97311099; PubMed-9166430;  RA MEDLINE-97311099; PubMed-9166430;  RF Liao F., Alkhatib G., Peden K.W., Sharma G., Berger E.A., FR  FI STRL33, A novel chemokine receptor like protein, functions  RT fusion cofactor for both macrophage-tropic and T cell line-i |
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
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EMBL; AF084229; AAD52041.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                   SEQUENCE
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"Sequences and Predicted
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=STRL33(BONZO);
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    MAY-2000 (TERMBLrel. 13, Created)
    MAY-2000 (TREMBLrel. 11, Last sequence update)
    T-UN-2002 (TERMBLrel. 21, Last annotation update)
    protein-coupled receptor STRL33

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181 GYHDEAISTVVLATQMTLGFFLPLLIMIVCYSVIIKTLLHAGGFQKHRSLKIIFLVMAVF
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Poehlmann S., Lee B., Meister S., Kirchhoff F.; Submitted (FEB-2000) to the EMBL/G EMBL, AF237559; AAF68392.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
SEQUENCE 343 AA; 39589 MW; A75B7A0751C13455 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro: IPR000276; GPCR_Rhodpsn. pfam; pr00001; 7tm_1; 1. PR1WTS; PR00237; GPCRRHODOPSN. PRINTS; PR01568; LYMPHOTACTNR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pohlmann S., Lee Kirchhoff F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Simian immunodeficiency virus utilizes not rhesus macaque STRL33 for efficient J. Virol. 74:5075-5082(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=20261727;
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WKLVKDIGCLPYLGVSHQWKSSEDNSKTFSASHNVEATSMFQL
                                                             LTCITVDRFIVVVKATKAYNQQAKRMTWGKVTSLLIWVISLLVSLPQIIYGNVFNLDKLI
                                                                                                                                                                                                                                                                                                                        LTCTTVDRFIVVVKATKAYNQQAKRMTWGKVICLLIWVISLLVSLPQIIYGNVFNLDKLI
                                                                                                                                                                                                                                                          HKLQSLTDVFLVNLPLADLVFVCTLPFWAYAGIHEWIFGQVMCKTLLGVYTINFYTSMLI
                                                                                                                                                                                                                                                                         HKLQSLTDVFLVNLPLADLVFVCTLPFWAYAGIHEWVFGQVMCKSLLGIYTINFYTSMLI
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                                                                                                                                                            CGYHDEAISTVVLATQMTLGFFLPLLTMIVCYSVIIKTLLHAGGFQKHRSLKIIFLVMAV
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a., Meister S., K
                                                                                                                                                                                                                                                                                                                                                                                                  94.3%;
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Last sequence up
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Pred. No. 6.26
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entry
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RESULT
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Best Local
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                                                   O9EQ16

O9EQ16;

O1-MAR-2001 (TrEMBLrel. 1)

O1-MAR-2001 (TrEMBLrel. 1)

O1-JUN-2002 (TrEMBLrel. 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9BDS6;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
02-phan seven transmembrane receptor STRL33.
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wade-Evans A.M., Russell J., Jenkins A., Javan C.; "Cloning and sequencing of cynomolgus macaque ccr3, potential coreceptors for HIV type 1, HIV type 2, au AIDS Res. Hum. Retroviruses 17:371-375(2001). EMBL; AF291671; AAK25742.1;
                                         Chemokine
   Eukaryota;
Mammalia; I
                         Mus
                                  CXCR6
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Receptor; Transmembrane. SEQUENCE 343 AA; 3947
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Pfam; PF00001; 7tm_1; 1.
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                        musculus (Mouse)
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  ; Metazoa;
Eutheria;
                                            receptor
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 Chordata;
Rodentia;
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16,
21,
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Last sequence Last anno
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Pred. No. 9.1e
9; Mismatches
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Craniata; Vertebrata;
Sciurognathi; Muridae
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                                                    sequence update)
annotation update)
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  Muridae;
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and SIV.";
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             Euteleostomi;
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  Murinae;
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RESULT
Q9ERH5
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Best Local S
Matches 258
"Molecular cloning of a putative (expressed in mouse lymphocytes."; Submitted (SEP-2000) to the EMBL/(SEMBL, AF305709; AAG31284.1; -MGD; MGI:1934582; Cxcr6.
Interpro; IPR000276; GPCR_Rhodpsn
                                                                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10090;
                                                                                                                                                                                                                     O9ERH5
O9ERH5;
01-MAR-2001 (TIEMBLrel 16,
01-MAR-2001 (TIEMBLrel 16,
01-JUN-2002 (TIEMBLrel 21,
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SEQUENCE
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PRINTS; PR01568; LYMPHOTACTNR.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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                                                                                STRAIN-C57BL/6; TIS
Sato H., Taniguchi
                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                          Putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:1934582; Cxcr6.
InterPro; IPR000276; GPCR_Rhodpsn
Pfam; PF00001; 7tm_1; 1.
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MEDLINE=21177382; PubMed=11017100;
... David A., Engel S.,
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                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                              CXCR6
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258; Conserv
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                                                                                                TISSUE-SPLEEN;
                                                                                                                                                                                                           receptor
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                                                                                                                                                                                                                                   Created)
                                           EMBL/GenBank/DDBJ
                                                                                                                                                                                                                       Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1332; D: Pred. No. 5.8e 86; Mismatches
                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                    chemokine
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Pfam; PF00001;

7tm\_1;

GPCRRHODOPSN

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Qy
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DR
KW
SQ
                                                                                                                                              Query Match
Best Local S
Matches 149
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Best Local S
Matches 257
                                                                                                                                                                                                                                       Receptor.
NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Human and ape molecular clocks hypotheses.";
                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF354630; AAL56234.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gorilla gorilla (gorilla).
Eukaryota; Metazoa; Chorda
Mammalia; Eutheria; Primat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Receptor.
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PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                             PROSITE; PS50262;
                                                                                                                                                                                                                                                                                                                                                       PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. Stauffer R.L., Wal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8WNM8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8WNM8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
mes 257; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                        Hered. 92:0-0(2001).
              232
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                                                                                                                                                al Similarity
149; Conserv
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; PS00337; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
; PS50262; G_PROTEIN_RECEP_F1_2; 1.
TYFLVMAVFLLTQMPFNLMKFIRSTHWEYYAMTSFHYTIMVTEAIAYLRACLNPVLYAFV
                                                                          VFNLDKLICGYHDEAISTVVLATQMTLGFFLPLLTMIVCYSVIIKTLLHAGGFQKHRSLK
                                                     VFNLDKLICGYHDEAISTVVLATQMTLGFFLPLLTMIVCYSVIIKTLLHAGGFQKHRSLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WKLMKDIGCLSHLGVSSQWKSSEDSSKTCSASHNVETTSMFQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WKLVKDIGCLPYLGVSHQWKSSEDNSKTFSASHNVEATSMFQL 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FLLTQMPFNLMKFIRSTHWEYYAMTSFHYTIMVTEAIAYLRACLNPVLYAFVSLKFRKNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGYHDEAISTVVLATQMTLGFFLFLLTMIVCYSVIIKTLLHAGGFQKHRSLKIIFLVMAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LTCITVDRFIVVVQATKAFNRQAKWKIWGQVICLLIWVVSLLVSLPQIIYGHVQDIDKLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LTCITYDRFIYVVKATKAYNQQAKRWTWGKVTSLLIWVISLLVSLPQIIYGNVFNLDKLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FLLTQTPFNLAMLIQSTSWEYYTITSFKYAIVVTEAIAYFRACLNPVLYAFVGLKFRKNV
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                                                                                                                                                                                                                                       150
150 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 351 AA;
                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                        G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                       150
17352
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Primates;
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                                                                                                                                                                   43.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73.9%;
                                                                                                                                                                                                                                       MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36;
                                                                                                                                              0;
                                                                                                                                              Score 783; DB Pred. No. 1.1e 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1326; DB 11;
Pred. No. 1.8e-102;
6; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                       C5427C09AB0502E9
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and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lyons-Weiler constraints
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                                                                                                                                                                                          DB
                                                                                                                                                                     .1e-57;
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                                                                                                                                                                                          Length 150;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
Gorilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    351
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                                                                                                                                              0,
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       RESULT
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ID Q9
AC Q9
DT 01
DT 01
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DT 01
DT 01
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Q8WNM7
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Best Local
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Q9UQQ6;
01-MAY-2000
01-MAY-2000
01-JUN-2002
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                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                       CCR9.
                                                                                                                                                                                                                                                            Chemokine
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01-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Receptor.
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=99248139; PubMed=10229797;
Zaballos A., Guttierrez J., Varona R., Ar.
"Identification of the orphan chemokine
"Identification of the orphan TECK.";
                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Hered. 92:0-0(2001).
EMBL; AF354631; AAL56335.1; -
INTERPROPORTS; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Stauffer R.L., Walker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pongo pygmaeus (Orangutan).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Human and ape molecular hypotheses.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9600;
                                                                                                                                                                                                                                                                                                                                                                                                                  al Similarity
147; Conserv
                                                                                                                                               000 (TrEMBLrel. 13, 0
000 (TrEMBLrel. 13, 1
002 (TrEMBLrel. 21, 1
002 (TrEMBLrel. 21, 1
                                                                                                                                                                                                                                                                    PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLKFRKNFWKLVKDIGCLPYLGVSHQWKSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.
149
149 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 20, Created)
(TrEMBLrel. 20, Last sequence up
(TrEMBLrel. 21, Last annotation
                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                        (Human)
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149
17256 N
                                                                                                Chordata;
Primates;
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98.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W.
                                                                                                                                               Created)
Last sequence update)
Last annotation update)
chemokine receptor 9A).
                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 771; טב כ,
                                                                                                Craniata; V. Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Pongo.
                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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and
                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                          369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      149
                                     Ardavin
                                                                                                             Vertebrata;
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|--------------------|--------------------|--------------------|--------------------|----------|----------|--------------------|----------|--------------------|--------------------|--------------------|----------------------|--------------------|----------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|--------------------|----------|----------|----------|-------------|-------------|----------|-------------|--------------------|----------|-------------------|
| ω<br>·             | ω.                 | 33.8               | w                  | ω.       | ω<br>·   | ω                  | ω        | ω.                 | ω                  | ω.                 | ω                    | ω.                 | ω.       | ω.                 | ω.                 | ω.                 | ω        | ω                  | ω.                 | ω.                 | ω.                 | w                  | 4.       | 4.                 | ٠        | 4        | 4.       | 4.          | ٠.          | 8        | 4.          | 5                  |          | 96.4              |
| 369                | 359                | 359                | 359                | 359      | 357      | 569                | 410      | 410                | 410                | 410                | 378                  | 378                | 378      | 378                | 378                | 378                | 378      | 378                | 378                | 358                | 358                | 358                | 369      | 357                | 357      | 357      | 374      | 374         | 369         | 302      | 351         | 342                | 342      | 342               |
| 22                 | 23                 | 21                 | 19                 | 15       | 21       | 22                 | 23       | 21                 | 19                 | 15                 | 23                   | 23                 | 22       | 22                 | 21                 | 21                 | 21       | 19                 | 15                 | 23                 | 21                 | 15                 | 22       | 22                 | 21       | 21       | 23       | 22          | 22          | 19       | 20          | 22                 | 20       | 22                |
| ABB56344           | AAU91233           | AAB21691           | AAW48728           | AAR53747 | AAY90649 | ABG12373           | AAU91229 | 89                 | AAW48723           | 74                 | AAU91241             | AAU91230           | AAB50859 | AAG80114           | AAY90629           | AAB21699           | AAB21688 | AAW48724           | AAR53744           | AAU91231           | AAB21689           | AAR53745           | AAG80116 | AAG80117           | AAY90615 | AAB19605 | ABB09291 | AAG80112    | AAG80113    | AAW70001 | AAY23825    | AAU04033           | AAW97784 | AAU04034          |
| Non-endogenous hum | Mouse 7 transmembr | Murine 7TM recepto | Murine V31 seven t | emb      | _        | Novel human diagno |          | Genomic clone of 7 | Polypeptide sequen | Putative seven tra | . Mouse 7 transmembr | Human 7 transmembr |          | Human CCR7 protein | Human G protein-co | 7TM receptor prote |          | Human V31 seven tr | Putative seven tra | Human 7 transmembr | Human 7TM receptor | Partial sequence o | prote    | Human CCR9b protei |          | Ħ.       | kine (   | CCR6a prote | CCR6b prote | dent ch  | es membrane | Green monkey SIV t | ican gr  | Pigtailed macaque |

## ALIGNMENTS

RESULT 1
AAW80806
ID AAW8

AAW80806 standard; Protein; 342 AA

#### New isolated fusion accessory factor STRL33 - which mediates HIV infection of cells, used to develop products for the study, prevention and therapy of HIV-related disorders WPI; 1998-557107/47. N-PSDB; AAV68515. STRL33 protein sequence. AAW80806; Alkhatib G, 31-MAR-1997; 31-MAR-1998; 08-OCT-1998 WO9844098-A2 Homo sapiens. STRL33; human; HIV-1; HIV related 22-JAN-1999 (USSH ) US SEC HEALTH & HUMAN SERVICES fusion accessory factor. Berger (first entry) 97US-0042880. 98WO-US06517. ΕA, Farber JM, disorder; therapy; CD4; diagnosis; Liao H

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RESULT 2
AAW54041
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Best Local
WPI; 1998-208924/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                         anorexia; Parkinson's disease; acute heart failure; atheroscleros: osteoporosis; angina pectoris; myocardial infarction; psychotic dibenian prostatic hypertrophy; neurological disorder; therapy;
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                                                      Bergsma
                                                                                                                                                               26-SEP-1996;
                                                                                                                                                                                                                                                                           08-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7-transmembrane receptor; HBMBU14; infection; HIV; cancer;
                                                        DJ,
                                                                                                         SMITHKLINE BEECHAM CORP.
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RESULT 3 AAY39366

AAY39366 standard; Protein;

342

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05-JAN-2000

(first entry)

factor-4

(PF-4) receptor amino acid sequence

PF-4; platelet factor-4; alpha granules; coll thrombosis; inflammatory activity; chemokine; BONZO; TYMSTR; agonist; antagonist; HIV; AIDS

WO9950670-A1

Homo

sapiens

psoriasis;

HIV; AIDS; rheumatoid inflammatory disorder

collagen; thrombotic stimuli; kine; PF-4 receptor; HBMBU14; AIDS; rheumatoid arthritis;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence is the human HBMBU14 protein of the invention. HBMBU14 CC is a human 7-transmembrane (TM) receptor. The products can be used for CC treating or preventing conditions related to abnormal HBMBU14 expression CC or activity, e.g. infections such as bacterial, fungal, protozoan and CC viral infections especially infections caused by HTV-1 and HTV-2, pain, CC cancers, anorexia, bulimia, asthma, Parkinson's disease, acute heart CC failure, atherosclerosis, hypotension, hypertension, urinary retention, CC osteoporosis, angina pectoris, myocardial infarction, ulcers, asthma, CC allergies, benign prostatic hypertrophy and psychotic and neurological CC disorders, including anxiety, schizophrenia, manic depression, delirium, CC dementia or severe mental retardation, and dyskinesias, such as CC Huntington's disease or Gilles de la Tourette's syndrome. The products CC can also be used for diagnosing a disease or susceptibility to a disease crelated to the expression of HBMBU14 and for identifying compounds which CC bind to and activate or inhibit a receptor for the polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated human 7-trans-membrane receptor, HBMBU14 - useful developing products for treating, e.g. infections, pain, cancer anorexia, hypotension, osteoporosis and asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 12;
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                  KLVKDIGCLPYLGVSHQWKSSEDNSKTFSASHNVEATSMFQL
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                                                                                                                                                                                                          TCITVDREIVVVKATKAYNQQAKRMTWGKVTSLLIWVISLLVSLPQIIYGNVFNLDKLIC
                                                                                        LLTQMPFNLMKFIRSTHWEYYAMTSFHYTIMVTEAIAYLRACLNPVLYAFVSLKFRKNFW
                                                                                                                                         GYHDEAISTVVLATQMTLGFFLPLLTMIVCYSVIIKTLLHAGGFQKHRSLKIIFLVMAVF
                                                                                                                                                                                                                                                                                MAEHDYHEDYGFSSFNDSSQEEHQDFLQFSKVFLPCMYLVVFVCGLVGNSLVLVISIFYH 60
                                                                                                                                                                                                                                                                                                                 KLQSLTDVFLVNLPLADLVFVCTLPFWAYAGIHEWVFGQVMCKSLLGIYTINFYTSMLIL
KLVKDIGCLPYLGVSHQWKSSEDNSKTFSASHNVEATSMFQL
                                                                     LLTQMPFNLMKFIRSTHWEYYAMTSFHYTIMVTEAIAYLRACLNPVLYAFVSLKFRKNFW
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       when platelets are activated by contacting collagen or other thrombotic stimuli. PF-4 promotes thrombosis at sites of platelet activation, and also exhibits several inflammatory activities. The carboxy terminal tridecapeptide of PF-4 is a potent chemotactic agent for monocytes. PF-4 is a cXC chemokine. The PF-4 receptor, also known as HBMBU14, TWMSTR and BONZO. is used in the methods of the invention. The invention relates to a novel screening method for identifying antagonists and agonists of the PF-4 receptor, involving using PF-4 and the PF-4 receptor to the receptor are used to identify further chemokine ligands for the receptor using a competitive binding assay and labelled PF-4. PF-4 is used to identify neutralizing or activating antibodies to the PF-4 can be used for therapy. PF-4 can be used in a screening method for identifying an antagonist of the receptor. Antagonists and agonists may be used for therapeutic purposes, such as treatment of HIV, AIDS, rehematory diseases
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Matches 342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence is the platelet factor-4 (PF-4) receptor amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel PF-4 receptor assays used to identify antagonists and agonists the receptor for use in therapy \,
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                                                                                                                                             GYHDEAISTVVLATQMTLGFFLPLLTMIVCYSVIIKTLLHAGGFQKHRSLKIIFLVMAVF
                                                                              LLTQMPFNLMKFIRSTHWEYYAMTSFHYTIMVTEAIAYLRACLNPVLYAFVSLKFRKNFW
                                                                                                                                                                                                                                                                       KLQSLTDVFLVNLPLADLVFVCTLPFWAYAGIHEWVFGQVMCKSLLGIYTINFYTSMLIL
KLVKDIGCLPYLGVSHQWKSSEDNSKTFSASHNVEATSMFQL
                               KLVKDIGCLPYLGVSHQWKSSEDNSKTFSASHNVEATSMFQL 342
                                                                                                                            GYHDEAISTVVLATQMTLGFFLPLLTMIVCYSVIIKTLLHAGGFQKHRSLKIIFLVMAVF
                                                                                                                                                                                          TCITVDRFIVVVKATKAYNQQAKRMTWGKVTSLLIWVISLLVSLPQIIYGNVFNLDKLIC
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                                                             LLTQMPFNLMKFIRSTHWEYYAMTSFHYTIMVTEAIAYLRACLNPVLYAFVSLKFRKNFW
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Pred. No. 1.4e-180;
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RESULT 4
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AAW97783 standard;

Protein; 342

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61 KLQSLTDVFLVNLPLADLVFVCTLPFWAYAGIHEWVFGQVMCKSLLGIYTINFYTSMLIL 120

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This is the amino acid sequence of human Bonzo, a novel HIV/SIV translocation promoting agent that acts in conjunction with CD4 to serve as a receptor for the entry into a cell of a virus having a specific viral envelope glycoprotein. Bonzo is a member of the receptor family, and is expressed in related to the chemokine receptor family, and is expressed in lymphoid tissues. The invention provides the amino acid sequences (see AAW07289-94) of human, African green monkey and pig-tailed macaque Bonzo and Bob (brother of Bonzo) translocation promoting agents. These novel receptors were identified using an expression cloning stategy. They were found to be used by particular strains of HIV-2 and M-tropic HIV-1. The invention also includes: mammalian cells transfected with Bonzo and/or Bob and human CD4, which can be used to screen potential therapeutic agents and identify ligands; antibodies to Bonzo, which can be used therapeutically, e.g. as antagonists or to target toxins or radioisotopes to HIV-permissive cells; transgenic
                                                                                             Query Match
Best Local S
Matches 342
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                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid encoding the human translocation promoter Bonzo used to screen for potential agents for treating acquired immune
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                                                                                                                                                                                                                                                          used therapeutically, particularly expressed from a gene therapy
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                                                                                                                   Local Similarity
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Kewalramani VN,
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                                                                                                                   100.0%; Score 1794; DB 20; 100.0%; Pred. No. 1.4e-180;
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RESULT 5
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or prostatic), organ rejection, inflammation and autoimmune diseases.
Also inhibitors of (I) are used therapeutically against tumors (and their metastases), inflammation (particularly bronchial asthma or chronic bowel inflammation), or autoimmune diseases (rheumatoid arthritis or lupus), where the (cardio)vascular, lymphatic, respiratory, nervous, digestive, endocrine, motor or urogenital systems or skin are affected, and bone marrow diseases. The products of the invention are chemokine derivatives which have cytostatic, antiinflammatory, antiasthmatic, inflammatory cells through a chemokines act on specific tumor and inflammatory cells through a constellation of chemokine receptors (CR), which control migration and
                                                                                                                                                                                                                                                                  Diagnostic agent cont useful for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection; inflammation; autoimmune disease; metastasis; bronchial asthma; lupus; chronic bowel inflammation; rheumatoid arthritis; cytostatic; antiinflammatory; antiasthmatic; immunosuppressive; dermatological;
                                                                                                                                                                                                                                                                                                                       WPI; 2001-626256/72.
                                                                                                                                                                                                                                                                                                                                                                                 (IPFP-)
(FORS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiinflammatory; antiaschmacantirheumatic; antiarthritic.
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                                                                                                                                                                         disease.
                                                                                                                                                                                                                                 Disclosure;
                                                                                                                                                                                                                                                                                                                                                   Forssmann W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-APR-2001; 2001WO-EP03708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human CXCR6 protein.
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                                                                                                                                                                 s invention describes a novel diagnostic agent (A) comprising at leas different ligands (I) for receptors (II) that are implicated in ease. (A) are used for the diagnosis of tumors (especially colorectal
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                                                An antibody for the treatment or prevention of HIV-infection a gpl20 portion which binds to DC-SIGN or is exposed upon gpl of DC-SIGN due to concomitant conformational change - \,
                                                                                                                               (UYNY )
                                                                                                                                                                                                                                                           Human; receptor; DC-SIGN; der
gp120; C-type lectin; ICAM3;
HIV infection.
           The specification
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                                                                                                            Littman
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                                                                                                                                                                                                                      Human; chemokine receptor; CCR11; G protein coupled receptor; inflammatory disease; rheumatoid arthritis; inflammatory bowel disease; asthma; angiogenesis; artherosclerosis vascular association disease; hypertension; angina pectoris; cardiac arrhythmia; Raynaud's phenomenon; left ventricular diastolic dysfunction; migraine; preterm labour; oesophageal spasm; ischaemic stroke; subarachnoid haemorrhage;
                                                                                                                                                                Homo
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myocardial infarction; congestive heart
vasospasm; retinopathy; nephropathy; pu
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03-MAR-2000;
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                                                                                                                                                                                                                                                                                                             expressing human CD4 and primate Bonzo or BOB (Brother Of Bonzo), contacting the cell with a virus pseudotyped with an HIV envelope glycoprotein, and measuring the cell's ability to resist infection. method is useful for selecting or identifying an agent, which can be method is useful for selecting or identifying an agent, which can be
                                                                                                                                                                                                                                                                            Sequence
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Best Local Similarity
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                                                                                                                             TCITVDRFIVVVKATKAYNQQAKRMTWGKVTSLLIWVISLLVSLPQIIYGNVFNLDKLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of a
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Pred. No. 1.4e-180;
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                                                                    of Bonzo) translocation promoting agents. These novel receptors were identified using an expression cloning stategy. They were found to be used by particular strains of HIV-2 and M-tropic HIV-1. The invention also includes: mammalian cells transfected with Bonzo and/or Bob and human CD4, which can be used to screen potential therapeutic agents and identify ligands; antibodies to Bonzo, which can be used therapeutically, e.g. as antagonists or to target toxins or radioisotopes to HIV-permissive cells; transgenic
                                                                                                                                                                                   This is the amino acid sequence of pig-tailed macaque Bonzo, a novel HIV/SIV translocation promoting agent that acts in conjunction with CD4 to serve as a receptor for the entry into a cell of a virus having a specific viral envelope glycoprotein. Bonzo is a member of the 7-transmembrane G-protein coupled receptor family, is closely related to the chemokine receptor family, and is expressed in lymphoid tissues. The invention provides the amino acid sequences (see AAW97783-88) and DNA sequences (see AAX07289-94) of human, frican green monkey and pig-tailed macaque Bonzo and Bob (brother translocation action accounts and bob (brother translocation).
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Sequence
                                                                                                                                                                                                                                                                                                                                            Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid encoding the human translocation promoter Bonzo to screen for potential agents for treating acquired immune
                                         therapeutically,
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                                         e and ribozyme molecules, which may particularly expressed from a gene
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chemokine receptor; AIDS; infection;
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Query Match Best Local Similarity

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Score Pred.

1730; No. 86 0; DB 2 8e-174;

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RESULT 11
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The sequence represents a novel SIV (Simian immunodeficiency virus translocating agent, Bonzo. The invention relates to selecting and that may be used in treating acquired immunodeficiency syndrome (comprises administering a potential therapeutic agent to a cell expressing human CD4 and primate Bonzo or BOB (Brother Of Bonzo), contacting the cell with a virus pseudotyped with an HIV envelope glycoprotein, and measuring the cell's ability to resist infection method is useful for selecting or identifying an agent, which can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pigtailed macacque; Bonzo; simian immunoder SIV translocating agent; CD4; BOB; Brother agent age
                                                                                                                                                                                                                                                                                                                                                                                               AIH
                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying an agent for treating potential therapeutic agent to a Bonzo or BOB and contacting the
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)B; AAS07616.
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Best Local
This is the amino acid sequence of African green monkey Bonzo, a novel HIV/SIV translocation promoting agent that acts in conjunction with CD4 to serve as a receptor for the entry into a cell of a virus
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Pred. No. 8e-174;
7; Mismatches 8;
                                                                                                           English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₽
                                                                                                                                                                                                                                                                                                                                                 DR,
                                                                                                                                                                                    translocation promoter Bonzo for treating acquired immune
                                                                                                                                                                                                                                                                                                                                              Unutmaz
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RESULT 13
AAU04033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chaving a specific viral envelope glycoprotein. Bonzo is a member of the 7-transmembrane G-protein coupled receptor family, is closely crelated to the chemokine receptor family, and is expressed in lymphoid tissues. The invention provides the amino acid sequences (see AAW9789-94) of human, for the form of the following sequences (see AAW9789-94) of human, for the following and post coupled macaque Bonzo and Bob (brother of Bonzo) translocation promoting agents. These novel receptors were identified using an expression cloning stategy. They were found to be used by particular strains of HIV-2 and M-tropic HIV-1. The invention also includes: mammalian cells transfected with Bonzo and/or Bob and human CD4, which can be used to screen potential therapeutic agents and identify ligands; antibodies to Bonzo, which can be used therapeutically, e.g. as antagonists or to target toxins or radioisotopes to HIV-permissive cells; transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local s
Matches 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    animals; and antisense and ribozyme molecules, which may also be used therapeutically, particularly expressed from a gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local -
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                                                                                                                                                                        241 LLTQMPFNLMKFIRSTHWEYYAMTSFHYTIMVTEAIAYLRACLNPVLYAFVSLKFRKNFW
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                                                                                                   KLVKDIGCLPYLGVSHQWKSSEDNSKTFSASHNVEATSMFQL 342
                                                                                                                                                                                                                            GYHDEEISTVVLATQMTLGFFLPLLAMIVCYSVIIKTLLHAGGFQKHRSLKIIFLVMAVF
                                                                                                                                                                                                                                                GYHDEAISTVVLATQMTLGFFLPLLTMIVCYSVIIKTLLHAGGFQKHRSLKIIFLVMAVF
                                                                                                                                                                                                                                                                                                                    TCITVDRFIVVVKATKAYNQQAKRMTWGKVTSLLIWYISLLVSLPQIIYGNVFNLDKLIC
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                                                                                    KLVKDIGCLPYLGVSHQWKSSEDNSKTFSASHNVEATSMFQL
                                                                                                                                                        LLTQTPFNLVKLIRSTHWEYYAMTSFHYTIIVTEAIAYLRACLNPVLYAFVSLKFRKNFW
                                                                                                                                                                                                                                                                                                 TCITVDRFIVVVKATKAYNQQAKKMTWGKVICLLIWVISLLVSLPQIIYGNVFNLDKLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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95.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1717; DB 20;
Pred. No. 1.9e-172;
9; Mismatches 7;
AΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 342;
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AAU04033 standard; Protein; 342

# AAU04033

23-OCT-2001 (first entry)

Green monkey SIV translocation agent, Bonzo.

Monkey; Bonzo; simian immunodeficiency virus; SIV translocating agent; CD4; BOB; Brother of Bonzo; acquired immunodeficiency syndrome; AIDS; SIV; HIV.

Cercopithecus

aethiops

US6251582-B1

26-JUN-2001.

16-JUL-1998; 98US-0116498

17-JUL-1997; 97US-0052827

ACC XXX ACC XX

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RESULT 14
AAX73825
ID AAX7
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AC AAX7
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AC AAX7
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AC AAX7
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DT 15-9
DE A7 t 1
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Best Local S
Matches 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence represets a novel SIV (Simian immunodeficiency virus) translocating agent, Bonzo. The invention relates to selecting an agen that may be used in treating acquired immunodeficiency syndrome (AIDS) comprises administering a potential therapeutic agent to a cell expressing human CD4 and primate Bonzo or BD8 (Brother Of Bonzo), contacting the cell with a virus pseudotyped with an HIV envelope glycoprotein, and measuring the cell's ability to resist infection. The method is useful for selecting or identifying an agent, which can be u
                          JP11155573-A
                                                   Unidentified
                                                                                                            A7 times membrane
                                                                                                                                       15-SEP-1999
                                                                                                                                                                AAY23825;
                                                                                                                                                                                      AAY23825 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying an agent for treating AIDS comprises administering a potential therapeutic agent to a cell expressing human CD4 and prim Bonzo or BOB and contacting the cell with a virus pseudotyped with HIV envelope glycoprotein -
  15-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in treating AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Column 41-42; 41pp; English.
                                                                        7 times membrane-penetrating
leukocyte function; control;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYNY )
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26; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLQSLTDVFLVNLPLADLVFVCTLPFWAYAGIHEWVFGQVMCKSLLGIYTINFYTSMLIL
                                                                                                                                                                                                                                                                                                                                                                  GYHDEAISTVVLATQMTLGFFLPLLTMIVCYSVIIKTLLHAGGFQKHRSLKIIFLVMAVF
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                                                                                                                                                                                                                                                    KLVKDIGCLPYLGVSHQWKSSEDNSKTFSASHNVEATSMFQL
                                                                                                                                                                                                                                                                                                    KLYKDIGCLPYLGVSHQWKSSEDNSKTFSASHNVEATSMFQL 342
                                                                                                                                                                                                                                                                                                                                                      GYHDEEISTVVLATQMTLGFFLPLLAMIVCYSVIIKTLLHAGGFQKHRSLKIIFLVMAVF
                                                                                                                                                                                                                                                                                                                                                                                                       TCITVDRFIVVVKATKAYNQQAKKMTWGKVICLLIWVISLLVSLPQIIYGNVFNLDKLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            342 AA;
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                                                                                                           penetrating
                                                                                                                                                                                       Protein;
                                                                                                                                     entry)
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95.3%;
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Pred. No. 1.9e-172;
9; Mismatches 7;
                                                                        type receptor protein; drug.
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                                                                                                           type receptor
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                                                                                                           protein
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                                                                                                            ET60.
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Best Local S
Matches 258
                                                                        cellular morphology modification phosphoinositide lipid turnover; atrophy; 941D12.
                                                                                                          Chemokine; primate; human; rodent; chemokine receptor; asthma; inflammatory response; immune response; leukocyte migration; Gleukocyte adhesion; chemoattractant; modulation; antiviral res
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                              Rodent chemokine
                                                                                                                                                                                                                                       AAW70001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a 7 times membrane-penetrating type receptor protein ET60. The 7 times membrane-penetrating type receptor protein ET60 can be used for detecting a drug controlling the function of leukocyte.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 17-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New 7
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                        WO9832858-A2
                                                Mus sp.
                                                                                                                                                                                      20-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New 7 times membrane-penetrating type receptor protein ET60 - useful for detecting drug controlling function of leukocyte
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                                                                                                                                                                                                                                                                                                                                                                      FILTQMPFNLMKFIRSTHWEYYAMTSFHYTIMVTEAIAYLRACLNPVLYAFVSLKFRKNF 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                               WKLVKDIGCLPYLGVSHQWKSSEDNSKTFSASHNVEATSMFQL
                                                                                                                                                                                                                                                                                                                                                                                                                       CGYHDEAISTVVLATQMTLGFFLPLLTMIVCYSVIIKTLLHAGGFQKHRSLKIIFLVMAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HKLQSLTDVFLVNLPLADLVFVCTLPFWAYAGIHEWVFGQVMCKSLLGIYTINFYTSMLI 119
                                                                                                                                                                                                                                                                                                                                                                                                      CQYHSEEISTMVLVIQMTLGFFLPLLTMILCYSGIIKTLLHARNFQKHKSLKIIFLVVAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                     LTCITVDRFIVVVQATKAFNRQAKWKIWGQVICLLIWVVSLLVSLPQIIYGHVQDIDKLI
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                                                                                                                                                                                                                                                                                                    WKLMKDIGCLSHLGVSSQWKSSEDSSKTCSASHNVETTSMFQL
                                                                                                                                                                                                                                                                                                                                                     FLLTQTPFNLAMLIQSTSWEYYTITSFKYAIVVTEAIAYFRACLNPVLYAFVGLKFRKNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           351 AA;
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                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KASEI KOGYO
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                                                                                                                                                             receptor
                                                                                                                                                                                                                                       Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20pp; Japanese
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                                                                                                                                                            941D12 amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36; Mismatches
                                                                                                                                                                                                                                       302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1332; DB 20;
Pred. No. 7.5e-132;
                                                                                                                                                                                                                                       B
                                                                                              response; G-protein coupled
                                                                                    proliferation;
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248

308

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Gaps

83

regeneration;

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the invention exhibit structural properties of G-protein coupled creceptors (GPCR), although their ligands have not yet been identified. The chemokine and chemokine receptor polypeptides are useful to produce ligand:receptor complexes in vivo or in assay techniques. Assays may also involve chemical antagonists which block complex production or utilise competitive binding. Binding compounds identified (agonists or antagonists) can be used to modulate the physiological responses in cells (especially neurons, macrophages or lymphocytes) to treat e.g. abnormal proliferation, regeneration, generation and attrophy. The polypeptides are also used to produce antibodies useful diagnostically, for drug screening or for polypeptide purification. The polynucleotides are useful to produce probes for detecting the polypeptides, and to isolate the polypeptides or related sequences, especially from other species. They also allow transformation of cells for polypeptide production.
                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        therapeutically to treat conditions associated with abnormal physiology or development e.g. inflammatory conditions such as asthma. Chemokines are important in immune and inflammatory responses in that they induce leukocyte migration and adhesion. They are also chemoattractants for several cells involved in inflammation and can induce other biological responses e.g. modulation of second messenger levels (e.g. Ca++), cellular morphology modification responses, phosphoinositide lipid currover, possible antiviral responses etc. The chemokine receptors of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention provides novel primate and rodent chemokines and chemokine receptors. The chemokines, receptors and binding compounds (optionally antibodies/fragments specifically binding the chemokines) are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gorman DM,
Zlotnik A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rodent and primate chemokines and chemokine receptors - useful diagnostically and therapeutically to treat conditions associated with abnormal physiology or development e.g. inflammatory conditions \mathbf{v}
                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This represents a rodent chemokine receptor 941D12 amino acid sequence
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N-PSDB; AAV43795.
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                                      58.5%; Score 1049; DB 19; 72.2%; Pred. No. 4.2e-102;
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ALYDGHYEGDFWLFUNSSDNSQENKRFLKFKEVFLPCVYLVVFVFGLLGNSLVLIIYIFY 68

180 CGYHDEAISTVVLATQMTLGFFLPLLTMIVCYSVIIKTLLHAGGFQKHRSLKIIFLVMAV 239

CQYHSEEISTMVLVIQMTLGFFLPLLTMILCYSGIIKTLLHARNFQKHKSLKIIFLVVAV 248

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Search completed: July 15, Job time: 73 secs 2003, 07:18:36

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Post-processing: Minimum Match 0%
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length: 2000000000
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: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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US-09-852-156-7
US-09-966-755-2
US-10-251-385-24
US-10-252-567A-241
US-09-952-385-2
US-10-251-385-7
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| 45                | 44                | 43                | 42                | 41                 | 40              | 39                | 38                | 37                | 36              | 35                | 34                | ω                | 32              | 31                | 30                | 29                | 28                | 27                | 26              | 25              | 24               | 23              | 22                | 21                 | 20                |
|-------------------|-------------------|-------------------|-------------------|--------------------|-----------------|-------------------|-------------------|-------------------|-----------------|-------------------|-------------------|------------------|-----------------|-------------------|-------------------|-------------------|-------------------|-------------------|-----------------|-----------------|------------------|-----------------|-------------------|--------------------|-------------------|
| 512.5             | 512.5             | 512.5             | 520.5             | 520.5              | 520.5           | 521.5             | 521.5             | 521.5             | 521.5           | 521.5             | 522.5             | 522.5            | 524.5           | 524.5             | 524.5             | 524.5             | 524.5             | 527.5             | 527.5           | 527.5           | 560              | 560             | 560               | 560                | 560               |
|                   |                   | 28.6              | 29.0              | 29.0               | 29.0            | 29.1              | 29.1              | 29.1              | 29.1            | 29.1              |                   | 29.1             | 29.2            | 29.2              | 29.2              | 29.2              | 29.2              | 29.4              | 29.4            |                 |                  | 31.2            | 31.2              | 31.2               | 31.2              |
| 355               | 355               | 355               | 360               | 360                | 347             | 360               | 344               | 344               | 344             | 344               | 352               | 352              | 352             | 352               | 352               | 352               | 352               | 360               | 360             | 360             | 350              | 350             | 350               | 350                | 350               |
| 10                | 9                 | 9                 | 10                | 9                  | 10              | 10                | 10                | 10                | 9               | 9                 | 9                 | 9                | 10              | 10                | 9                 | 9                 | 9                 | 10                | 10              | 10              | 10               | 10              | 9                 | 9                  | 9                 |
| US-09-961-068-1   | US-10-245-850-2   | US-10-225-567A-62 | US-09-131-827A-2  | US-10-225-567A-460 | US-09-104-792-3 | US-09-131-827A-20 | US-09-779-880A-9  | US-09-779-879A-9  | US-10-067-800-9 | US-10-232-686-9   | US-09-870-759-144 | US-09-870-759-37 | US-09-953-717-2 | US-09-953-692-2   | US-10-245-850-1   | US-10-225-567A-76 | US-09-104-063-4   | US-09-938-703-7   | US-09-939-226-7 | US-09-938-719-7 | US-09-796-338A-8 | US-09-765-994-2 | US-10-288-222A-10 | US-10-225-567A-607 | US-10-282-837-8   |
| Sequence 1, Appli | Sequence 2, Appli |                   | Sequence 2, Appli |                    | 3, 1            | 20,               | Sequence 9, Appli | Sequence 9, Appli | 9,              | Sequence 9, Appli | Sequence 144, App | 7                | 2,              | Sequence 2, Appli | Sequence 1, Appli | Sequence 76, Appl | Sequence 4, Appli | Sequence 7, Appli | 7,              | 7,              | •                | e 2,            | ~                 | Sequence 607, App  | Sequence 8, Appli |

## ALIGNMENTS

US-10-225-567A-348

GENERAL INFORMATION:

Sequence 348, Application US/10225567A Publication No. US20030113798A1

Вb ΔÃ DЪ Qy Вþ 20 Ωy ; ORGANISM: HOMO US-10-225-567A-348 Query Match Best Local S Matches 342 APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPT FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: Patentin version 3.1
SEQ ID NO 348
LENGTH: 342 APPLICANT: LifeSpan Biosciences APPLICANT: Brown, Joseph P. TYPE: PRT Match 100.0%; Local Similarity 100.0%; nes 342; Conservative ( 181 121 121 61 61 GYHDEAISTVVLATQMTLGFFLPLLTMIVCYSVIIKTLLHAGGFQKHRSLKIIFLVMAVF TCITVDRFIVVVKATKAYNQQAKRMTWGKVTSLLIWVISLLVSLPQIIYGNVFNLDKLIC KLQSLTDVFLVNLPLADLVFVCTLPFWAYAGIHEWVFGQVMCKSLLGIYTINFYTSMLIL 120 KLQSLTDVFLVNLPLADLVFVCTLPFWAYAGIHEWVFGQVMCKSLLGIYTINFYTSMLIL TCITVDRFIVVVKATKAYNQQAKRMTWGKVTSLLIWVISLLVSLPQIIYGNVFNLDKLIC sapiens 0; Score 1794; DB 9; Pred. No. 9.8e-144; ); Mismatches 0; Length 342; Indels 0; Gaps 120 240 60 180 180 60 0;

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Patent No. US20020076694A1
                                                                                                                         Matches
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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                                                                                                                       Local Similarity
les 342; Conserv
                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: JACKSON ESG., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-009NCIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESSE: David A. Jackson,
ADDRESSEE: 411 Hackensack Ave, (
                                                                                                                                                                                                                             MOLECULE TYPE: pr
HYPOTHETICAL: NO
                                                                                                                                                                                                                 ORIGINAL SOURCE:
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                 61
                                          61
                                                                TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/852,156
FILING DATE: 09-May-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KLVKDIGCLPYLGVSHQWKSSEDNSKTFSASHNVEATSMFQL 342
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Ramani, Vineet N.K.
INVENTION: NOVEL ALTERNATIVE G-COUPLED RECEPTORS
ASSOCIATED WITH RETROVIRAL ENTRY INTO CELLS, METHODS
IDENTIFYING THE SAME, AND DIAGNOSTIC AND THERAPEUTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Littman, Dan
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 Sequence 6, Application US/09852156
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; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-940-063-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Briskin, Michael J.
APPLICANT: Murphy, Kristine E.
APPLICANT: Wilbanks, Alyson M.
APPLICANT: Wilbanks, Alyson M.
APPLICANT: Wilbanks, Dijun
TITLE OF INVENTION: No. US2002090657Alel Antibodies and Ligands for "Bonzo"
TITLE OF INVENTION: Chemokine Receptor
FILE REFERENCE: 1855.1070-000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 09/449,437
PRIOR FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 18
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SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2001-08-27
                         301 KLVKDIGCLPYLGVSHQWKSSEDNSKTFSASHNVEATSMFQL
                                                                                                              241 LLTQMPFNLMKFIRSTHWEYYAMTSFHYTIMVTEAIAYLRACLNPVLYAFVSLKFRKNFW 300
                                                                                                                                                                               181 GYHDEAISTVVLATQMTLGFFLPLLTMIVCYSVIIKTLLHAGGFQKHRSLKIIFLVMAVF
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342; Conserv
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KLVKDIGCLPYLGVSHQWKSSEDNSKTFSASHNVEATSMFQL
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                                                                                           LLTQMPFNLMKFIRSTHWEYYAMTSFHYTIMVTEAIAYLRACLNPVLYAFVSLKFRKNFW
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                           09-852-156-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 1049-1-009NCIP TELECOMMUNICATION INFORMATION: TELEPHONE: 201-487-5800 TELEPAX: 201-343-1684 INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: pigtail macaque SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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ADDRESSEE: David A. Jackson,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 342 amino acids
TYPE: amino acid
STRANDEDNESS: single
KLVKDIGCLPYLGVSHQWKSSEDNSKTFSASHNVEATSMFQL 342
                           LLTQMPFNLMKFIRSTHWEYYAMTSFHYTIMVTEAIAYLRACLNPVLYAFVSLKFRKNFW 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
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ASSOCIATED WITH RETROVIRAL ENTRY INTO CELLS; METHODS OF IDENTIFYING THE SAME, AND DIAGNOSTIC AND THERAPEUTIC US
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Ramani, Vineet N.K.
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Pred. No. 2.5e-138;
7; Mismatches 8;
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Sequence 4, Application US/09852156 Patent No. US20020076694A1 GENERAL INFORMATION:
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TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                       Local Similarity 95.3 es 326; Conservative
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APPLICATION NUMBER: US/09/852,156
FILING DATE: 09-May-2001
CLASSIFICATION: CLASSIFICATION: 
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: African Green Monkey SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Littman,
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                                                                TCITYDRFIVYVKATKAYNQQAKKMTWGKVICLLIWVISLLVSLPQIIYGNVFNLDKLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acids
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REFERENCE/DOCKET NUMBER: 1049-1-009NCIP
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ASSOCIATED WITH RETROVIRAL ENTRY INTO CELLS, METHODS OF IDENTIFYING THE SAME, AND DIAGNOSTIC AND THERAPEUTIC USE
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Ramani, Vineet
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95.3%;
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Pred. No. 3.1e-137;
9; Mismatches 7;
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              Sequence 2, Application US/09966755 Publication No. US20030022238A1 GENERAL INFORMATION:
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SEQ ID NO 390
LENGTH: 374
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APPLICANT: Andrew,
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APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
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APPLICANT: ROUSH, CHRISTINE L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
ILE REFERENCE: 1920-4-4
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                                                                                                                                                                                                                                                                                                                                                   192
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                                                                                                                                                                                                          HCCLNPVLYAFIGQKFRNYFLKILKDLWC----VRRKYKSSGFSCAGRYSENISRQTSE 362
                                                                                                                                                                                                                                                                                                             SLKIIFLVMAVFLLTQMPFNLM------KFIRSTHWEYYAMTSFHYTIMVTEAIAYL 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DYHEDYGFSSFNDSSQEEHQDFL-----QFSKVFLPCMYLVVFVCGLVGNSLVLVIS
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David P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.4%; Score 617; DB 9 36.3%; Pred. No. 2e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 9; Length 374;
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SEQ ID NO 2
LENGTH: 357
TYPE: PRT
ORGANISM: Homo sapiens
US-09-966-755-2
                                                                                                                    US-10-251-385-24
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Query Match
Best Local Similarity
Matches 123; Conserv
                                                                                                                                                                                                                     SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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Best Local
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APPLICANT: Ponath, Paul D.

TITLE OF INVENTION: ANTI-GPR-9-6 ANTIBODIES AND METHODS OF

TITLE OF INVENTION: IDENTIFYING AGENTS WHICH MODULATE GPR-9-6 FUNCTION

FILE REFERENCE: LKS98-16

GIRDBERN ASSESSMENTS.
                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/251,385
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: US/09/170,496
PRIOR FILING DATE: 1998-10-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Behan, Dominic P. APPLICANT: Chalmers, Derek T. APPLICANT: Liaw, Chen W.
                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US/09/266,464
PRIOR FILING DATE: 1999-03-11
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                SOFTWARE: PatentIn
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CURRENT FILING DATE: 2001-09-28
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                                                                                                                                      TYPE: PRT
ORGANISM: Homo
                                                                                                                                                                                            LENGTH:
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mes 123; Conserva
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ilarity 36.3%;
Conservative 8
        34.1%; Score 612; DB 9;
36.3%; Pred. No. 5.1e-44;
tive 82; Mismatches 100
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Pred. No. 5.1e-44;
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US-10-225-567A-241
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SEQ ID NO 241
LENGTH: 357
TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PEPTOR ADDRESS: 2001-12-19
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PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: Date: 2000: 2292
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                                                                                                                                                                                                                                                          YWYCTRVKTMTDMFLLNLAIADLLFLVTLPFWAIAAADQWKFQTFWCKVVNSMYKMNFYS
                                                                                                 SGIAICTMVYPSDESTKLKSAVLTLKVILGFFLPFVVMACCYTIIIHTLIQAKKSSKHKA
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                                                          LKIIFLVMAVFLLTQMPFNLMKFIRSTHWEYYAM-----TSFHYTIMVTEAIAYLRA
                                                                                                                        DDYG--SESTSSMEDYVNFNFTDFYCEKNNVRQFASHFLPPLYWLYFIVGALGNSLVILV
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                      LKVTITVLTVFVLSQFPYNCILLVQTI---DAYAMFISNCAVSTNIDICFQVTQTIAFFHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                         34.1%; Score 612; DB 9; 36.3%; Pred. No. 5.1e-44;
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CURRENT APPLICATION NUMBER: US/09/903,377
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/217,255
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/221,483
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: US 60/262,113
PRIOR APPLICATION NUMBER: US 60/262,113
PRIOR APPLICATION NUMBER: US 60/262,113
PRIOR FILING DATE: 2001-01-16
              GENERAL INFORMATION:
APPLICANT: Andrew, David P.
APPLICANT: Zabel, Brian A.
APPLICANT: Ponath, Paul D.
TITLE OF INVENTION: ANTI-GPR-9-6 ANTIBODIES AND METHODS
TITLE OF INVENTION: IDENTIFYING AGENTS WHICH MODULATE G
FILE REFERENCE: LKS98-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2 LENGTH: 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Allen, Keith D.
                                                                                                                                                       Sequence 2, Application US/09952385
Patent No. US20020119504A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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CURRENT APPLICATION NUMBER: US/09/952,385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 34.18;
Local Similarity 36.38;
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                                                                                                                                                                                                                                                                                                    CLNPVLYAFVSLKFRKNFWKLVKDIGCLPYLGVSHQWKS 320
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                                                                                                                                                                                                                                                                                                                                                            LKVTITVLTVFVLSQFPYNCILLVQTI--DAYAMFISNCAVSTNIDICFQVTQTIAFFHS
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Pred. No. 5.1e-44;
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                                         MODULATE GPR-9-6 FUNCTION
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US-10-000-759A-2
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Best Local S
Matches 123
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Patent No. US20020141991A1
GENERAL INFORMATION:
APPLICANT: Andrew, David P.
APPLICANT: Zabel, Brian A.
APPLICANT: Ponath, Paul D.
                                                              Matches
                                                                                      Query Match
                                                                                                                                                                     SEQ ID NO 2
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 2
LENGTH: 357
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                             APPLICANT: PONATH, PAUL D.
TITLE OF INVENTION: ANTI-GPR-9-6 ANTIBODIES
ITLE OF INVENTION: IDENTIFYING MODULATORS
ILE REFERENCE: 1855.1064-003
CURRENT APPLICATION NUMBER: US/10/000,759A
CURRENT FILING DATE: 2001-10-23
                                                                                                                                                                                NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US/09/522,752
PRIOR FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: US 09/266,464
PRIOR FILING DATE: 1999-03-11
                                                                                                                                           LENGTH: 35
TYPE: PRT
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PRIOR APPLICATION NUMBER: 09/266,464
PRIOR FILING DATE: 1999-03-11
                                                                        Local Similarity
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      DDYG--SESTSSMEDYVNFNFTDFYCEKNNVRQFASHFLPPLYWLVFIVGALGNSLVILV
                                 EDYGFSSFNDSSQEEHQDF---
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                                                                       Score 612; DB 12;
Pred. No. 5.1e-44;
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Pred. No. 5.1e-44;
                                                          Mismatches 100;
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; ORGANISM: Homo sapiens US-10-251-385-74
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US-10-251-385-74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local
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CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: US/09/170,496
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. US20030105292A1-Endogenous, Constitutively Activated Human
TITLE OF INVENTION: Protein-Coupled
TITLE OF INVENTION: Protein-Coupled
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
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TYPE: PRT
  348
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SQEQL-RQWSSCR-HIRRSSMSVEAETTTF
                                                                                                                KF-IRSTHWEYYAMTSFHYTIMYTEAIAYLRACLNPVLYAFVSLKFRKNFWKLVKDIGCL
                                                                                                                                                                                                                                                                                                                                                                                                                                    QDFLQFSKVFLPCMYLVVFVCGLVGNSLVLVISIFYHKLQSLTDVFLVNLPLADLVFVCT 83
                                        PYLGVSHQWKSSEDNSKTFSASHNVEATSMF
                                                                                NFNITSSTCELSKQLNIAYD--VTYSLACVRCCVNPFLYAFIGVKFRNDLFKLFKDLGCL
                                                                                                                                                             IGFLVPLLAMSFCYLVIIRTLLQARNFERNKAIKVIIAVVVVFIVFQLPYNGVVLAQTVA
                                                                                                                                                                                                     LGFFLPLLTMIVCYSVIIKTLLHAGGFQKHRSLKIIFLVMAVFLLTQMPFN-----LM
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Pred. No. 1.1e-43;
14; Mismatches 106
376
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US-10-251-385-176
, Sequence 176, Application US/10251385
, Publication No. US20030105292A1
, GENERAL INFORMATION:
, APPLICANT: Behan, Dominic P.
, APPLICANT: Chalmers, Derek T.
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US-10-225-567A-68
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 176
LENGTH: 357
                                                             APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. US20030105292A1-Endogenous, Constitutively Activated Human TITLE OF INVENTION: Protein-Coupled
TITLE OF INVENTION: Protein-Coupled
FILE REFERENCE: AREN-0040
CURRENT APPLICATION UNMEER: US/10/251,385
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION UNMBER: US/99/170,496
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
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SOFTWARE: PatentIn version 3.1
EQ ID NO 68
LENGTH: 378
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CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
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APPLICANT: ROUSH, Christine L.

TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
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US-09-116-498-7
US-09-116-498-8
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US-09-29-34-37B-19
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LENGTH: 342 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-742-011-2

Query Match Best Local S Matches 342

Local Similarity nes 342; Conserv

100.0%; Score 1794; DB 2; ilarity 100.0%; Pred. No. 1.6e-142; Conservative 0; Mismatches 0;

Length

342;

Gaps

60

TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 342 amino acids

OY B

61 KLQSLTDVFLVNLPLADLVFVCTLPFWAYAGIHEWVFGQVMCKSLLGIYTINFYTSMLIL 120

| Sequence 2, Application US/08742011 Sequence 2, Application US/08742011 Patent No. 5824504 GENERAL INFORMATION: APPLICANT: Elshourbagy, Nabil A. APPLICANT: Software E. COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION NUMBER: US/08/742,011 FILING DATE: CLASSIFICATION: 530 ATTORNEY/AGENT INFORMATION: NAME: Han, William T. REGESTRATION NUMBER: 34,344 REFERENCE/DOCKET NUMBER: ATG55020P | ALIGNMENTS | 28 606 33.8 359 4 US-09-088-337B-24 29 606 33.8 359 5 PCT-US93-11153-24 30 588.5 32.8 378 1 US-08-383-750-2 31 588.5 32.8 378 1 US-08-383-751A-2 32 588.5 32.8 378 4 US-09-045-583-49 34 588.5 32.8 378 4 US-09-534-185-49 35 588.5 32.8 378 5 PCT-US93-09639-2 36 568 31.7 350 2 US-08-966-316-18 37 560 31.2 350 2 US-08-966-316-18 37 560 31.2 350 2 US-08-966-316-18 38 554 30.9 361 2 US-08-966-316-18 39 554 30.9 361 2 US-08-965-37-2 40 527.5 29.4 360 4 US-09-178-637-2 41 524.5 29.2 352 1 US-08-076-093A-4 43 524.5 29.2 352 1 US-08-076-093A-4 44 524.5 29.2 352 2 US-08-284-586-4 45 524.5 29.2 352 2 US-08-805-478-4 |
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|  |            | Sequence 24, Appli<br>Sequence 24, Appli<br>Sequence 2, Appli<br>Sequence 2, Appli<br>Sequence 2, Appli<br>Sequence 49, Appli<br>Sequence 49, Appli<br>Sequence 16, Appli<br>Sequence 18, Appli<br>Sequence 2, Appli<br>Sequence 2, Appli<br>Sequence 2, Appli<br>Sequence 3, Appli<br>Sequence 4, Appli<br>Sequence 4, Appli<br>Sequence 4, Appli<br>Sequence 4, Appli<br>Sequence 4, Appli<br>Sequence 4, Appli  |

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RESULT 3
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       Sequence
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LENGTH: 342
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CURRENT FILING DATE: 1999-03-24
PRIOR APPLICATION NUMBER: 9806677.2
PRIOR ETLING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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APPLICANT: MOORES, KITTY
TITLE OF INVENTION: NEW I
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ORGANISM: HOMO SAPIENS
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        Application US/09116498
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Pred. No. 1.6e-142;
Mismatches 0;
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SEQUENCE DESCRIPTION: SEQ II
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GENERAL INFORMATION:
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TELEPAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 1049-1-009 TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
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                                                                                                KLVKDIGCLPYLGVSHQWKSSEDNSKTFSASHNVEATSMFQL 342
                                                 LLTQMPFNLMKFIRSTHWEYYAMTSFHYTIMVTEAIAYLRACLNPVLYAFVSLKFRKNFW
                                                                                                                                                                     TCITVDRFIVVVKATKAYNQQAKRMTWGKVTSLLIWVISLLVSLPQIIYGNVFNLDKLIC
                                                                                                                                                                                       TCITVDRFIVVVKATKAYNQQAKRMTWGKVTSLLIWVISLLVSLPQIIYGNVFNLDKLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 16-Jul-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
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STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 411 Hackensack Ave, Continental Plaza,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 342 amino acids
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                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INVENTION: NOVEL ALTERNATIVE G-COUPLED RECEPTORS
ASSOCIATED WITH RETROVIRAL ENTRY INTO CELLS, METHODS
IDENTIFYING THE SAME, AND DIAGNOSTIC AND THERAPEUTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07601
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Ramani, Vineet N.K.
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Pred. No. 1.6e-142;
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                          GENERAL INFORMATION:
APPLICANT: Littman, Dan R.
APPLICANT: Kwon, Douglas S.
APPLICANT: van Kooyk, Yvette
APPLICANT: egijtenbeck, Tneo
TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL
TITLE OF INVENTION: CELLS
FILE REFERENCE: 1049-1-017
CURRENT FILING DATE: 2000-03-02
RUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                Sequence 9, Application US/09517605
Patent No. 6391567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NO. 6319675el Antibodies
FILE OF INVENTION: Chemokine Receptor
FILE REFERENCE: 1855.1070-000
CURRENT APPLICATION NUMBER: US/09/449,437A
CURRENT FILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
                 SEQ ID NO 9
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LENGTH: 342
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Pred. No. 1.6e-142;
; Mismatches 0;
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GENERAL INFORMATION:
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               INFORMATION
                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Versi
SOFTWARE: Patentin Release #1.0, Versi
CURRENT APPLICATION NUMBER: US/09/116,498
FILING DATE: 16-Jul-1998
CLASSIFICATION: UNMBER: US/09/116,498
APPLICATION INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-009
TELECOMMUNICATION INFORMATION:
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les 342; Conserv
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ADDRESSEE: David A. Jackson
STREET: 411 Hackensack Ave,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unutmaz, Derya
Ramani, Vincet N.K.
TITLE OF INVENTION: NOVEL ALTERNATIVE G-COUPLED RECEPTORS
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SEQUENCE CHARACTERISTICS:
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STATE: New Jersey
COUNTRY: USA
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                             TELEPHONE: 201-487-58
TELEFAX: 201-343-1684
                 FOR SEQ ID NO: 6:
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Pred. No. 1.6e-142;
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                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION NUMBER: US/09/116,498
FILING DATE: 16-Jul-1998
CLASSIFICATION: CURROWN
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ADDRESSEE: David A. Jackson,
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HYPOTHETICAL: NO
ORIGINAL SOURCE:
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                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF
                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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                                                                                                                                                                                                      ZIP:
                                                                                                                                                                                                                                    CITY: Hackensack
STATE: New Jersey
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                   COUNTRY:
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Ramani, Vineet N.K.
INVENTION: NOVEL ALTERNATIVE G-COUPLED RECEPTORS
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Jackson Esq.,
                                                                                                                                                                                                                                                                              Floor
                                                                                                                                                                                                                                                                                          411 Hackensack
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95.6%;
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David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1730; DB 4;
Pred. No. 3.6e-137;
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                                                                                                                                                                                                                                                                                                                   Sequence 48, Application Patent No. 6287805 GENERAL INFORMATION:
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Best Local
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                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                      SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICATION NUMBER
                                          FILING DATE:
                                                         APPLICATION NUMBER:
                                                                                                                                                                  COUNTRY: UP
                                                                                                                                                                                                  STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
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SEQUENCE DESCRIPTION: SEQ
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STRANDEDNESS: single
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                                          20-MAR-98
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No. 6287805el Molecules
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95.3%;
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Pred. No. 4.4e-136;
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NO: 4:
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                                                                                                                                                                                                                                              Sequence 48, Application US/09534185
Patent No. 6403767
Patent No. 6403767
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
Heptahelical Receptor Superfamily and Uses
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tches 135; Conserva
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FRAGMENT TYPE:
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REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
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            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT
                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RACLNPVLYAFVSLKFRKNFWKLVKDIGCLPYLGVSHQWKS-----SEDNSKTFSA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AIRVIIAVVLVFLACQIPHNMVLLVTAANLGKMNRSCQSE----KLIGYTKTVTEVLAFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AFYKKARSMTDVYLLNMAIADILFVLTLPFWAVSHATGAWVFSNATCKLLKGIYAINFNC 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DSSEDY-FVSVNTSYYSVDSEMLLCSLQEVRQFSRLFVPIAYSLICVFGLLGNILVVITF 71
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                                                                                                                                                   CITY: Boston
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                                                                                                                   COUNTRY:
                                                                                                                                  STATE: Massachusetts
                                                                                                                                                                   ADDRESSEE: LAHIVE & COCKFIELD, LLP STREET: 28 State Street
                                                                                              ZIP: 02109
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APPLICATION DATA:
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Pred. No. 2.2e-44;
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Best Local
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; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-534-185-48
FILE REFERENCE: LKS98-16
CURRENT APPLICATION NUMBER: US/09/266,464
CURRENT FILING DATE: 1999-03-11
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 2
                                                                                                                                                                        Sequence 2, Application US/09266464
GENERAL INFORMATION:
APPLICANT: Andrew, David P.
APPLICANT: Zabel, Brian A.
APPLICANT: Ponath, Paul D.
TITLE OF INVENTION: AUTI-GPR-9-6 ANTIBODIES AND METHODS OF
TITLE OF INVENTION: IDENTIFYING AGENTS WHICH MODULATE GPR-9-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (617)742-4214 INFORMATION FOR SEQ ID NO: 48:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: peptide FRAGMENT TYPE: internal
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LENGTH: 374 amino ac
TYPE: amino acid
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REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)27-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         331 SHNVEATSMFQL 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     363 TADNDNASSFTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      252 AIRVIIAVVLVFLACQIPHNMVLLVTAANLGKMNRSCQSE----KLIGYTKTVTEVLAFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229 SLKIIFLVMAVFLLTQMPFNLM-------KFIRSTHWEYYAMTSFHYTIMVTEAIAYL 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192 QGSDVCEPKYQTVSEPIRWKLLMLGLELLFGFFIPLMFMIFCYTFIVKTLVQAQNSKRHK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72 AFYKKARSMTDYYLLNMAIADILFYLTLPFWAYSHATGAWYFSNATCKLLKGIYAINFNC 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 DSSEDY-FVSVNTSYYSVDSEMLLCSLQEVRQFSRLFVPIAYSLICVFGLLGNILVVITF 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RACLNPVLYAFVSLKFRKNFWKLVKDIGCLPYLGVSHQWKS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D-KLICGYHDEAIS-----TVVLATQMTLGFFLPLLTMIVCYSVIIKTLLHAGGFQKHR 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GMLLLTCISMDRYIAIVQATKSFRLRSRTLPRSKIICLVVWGLSVIISSSTFVFNQKYNT 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMLILTCITVDRFIVVVKATKAYNQQAKRMTWGKVTSLLIWVISLLVSLPQIIYGNVFNL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IFYHKLQSLTDVFLVNLPLADLVFVCTLPFWAYA-GIHEWVFGQVMCKSLLGIYTINFYT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DYHEDYGFSSFNDSSQEEHQDFL------QFSKVFLPCMYLVVFVCGLVGNSLVLVIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HCCLNPVLYAFIGQKFRNYFLKILKDLWC-----VRRKYKSSGFSCAGRYSENISRQTSE 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 09/045,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/534,185 FILING DATE: 24-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Mandragouras, Amy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION DATA:
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36.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 619; DB 4; Length 374; Pred. No. 2.2e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---SEDNSKTFSA 330
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Indels Length 358;

19;

Gaps

8

150

209

90

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RESULT 11
US-08-153-848-19
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                  INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: No. 5759804and; Greta E.
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
                                                                                    TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 64
                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                     TELEFAX: (J. TELEFAX: 25-3856
                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U:
ZIP: 60606
                                                                                                                                                                                                                                                         CLASSIFICATION: 514
                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 6300 :
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Marshall
ADDRESSEE: Bicknell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 CVLLIMCISVDRYIAIAQAMRAHTWREKRLLYSKMVCFTIWVLAAALCIPEILYSQIKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 YWYCTRVKTMTDMFLLNLAIADLLFLVTLPFWAIAAADQWKFQTFMCKVVNSMYKMNFYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLNPVLYVFVGERFRRDLVKTLKNLGCIS----QAQWVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LKVTITVLTVFVLSQFPYNCILLVQTI--DAYAMFISNCAVSTNIDICFQVTQTIAFFHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGIAICTMVYPSDESTKLKSAVLTLKVILGFFLPFVVMACCYTIIIHTLIQAKKSSKHKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DDYG--SESTSSMEDYVNFNFTDFYCEKNNVRQFASHFLPPLYWLVFIVGALGNSLVILV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6300 Sears Tower, 233 South Wacker Drive
358 amino acids
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Schweikart, Vicki L.
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                                                                       474-0448
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                                                                                                                                                                                                                                                                                         US/08/153,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5759804el Seven Transmembrane Receptors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gerstein, Murray
                                                                                                                                                                                                                                                                                                                                Version #1.25
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US-09-299-843A-19
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               ADDA:
STREET: 00.0
CITY: Chicago
CITY: Illinois
THATE: TISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                            ATTORNEY/AGENT INFORMATION:
                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                       APPLICATION NUMBER: US 08 FILING DATE: 17-NOV-1993
                                                                                                                                                          APPLICATION NUMBER: US 0 FILING DATE: 01-JUN-1998
                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC OPERATING SYSTEM:
REGISTRATION
                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               328 SQEQL-RQWSSCR-HIRRSSMSVEAETTTTF 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                         IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Marshall, O'Toole, Gerstein, Murray &
NUMBER:
                                                                                                                                                                                                                                                                                                            PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.9%; Score 608.5; DB 1 36.9%; Pred. No. 1.6e-43;
                                                                                                                          US 08/153,848
                                                                                                                                                                               US 09/088,337
                                                                                                                                                                                                                                                       US/09/299,843A
43,213
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US-09-088-337B-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19, Application US/09088337B Patent No. 6348574 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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TELECOMMUNICATION INFORMATION:
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                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088,337B
FILING DATE: 01-Jun-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/153,848
FILING DATE: 17-NOV-1993
                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 66 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Godíska, Ronald
Gray, Patrick W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     328 SQEQL-RQWSSCR-HIRRSSMSVEAETTTTF 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    251 KF-IRSTHWEYYAMTSFHYTIMVTEAIAYLRACLNPVLYAFVSLKFRKNFWKLVKDIGCL 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       198 LGFFLPLLTMIVCYSVIIKTLLHAGGFQKHRSLKIIFLVMAVFLLTQMPFN-----LM 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 QDFLQFSKVFLPCMYLVVFVCGLVGNSLVLVISIFYHKLQSLTDVFLVNLPLADLVFVCT
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                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                               CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLLISKLSCVGIWILATVLSIPELLYSDLQRSSSEQAMRCSLITEHVEAFITIQVA-QMV 209
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                                                                                                                                                                                                                                                                                                    ZIP: 60606
                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                          STREET: 6300 Sears Tower,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             358 amino acids
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36.9%;
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Pred. No. 1.6
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                                                                                                                                                                                                                                                                                                                                                                                             233 South Wacker Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19, Application PC/TUS9311153 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 122;
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INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                          STREET: Chicago
CITY: Chicago
Illinois
                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: NO NUMBER OF SEQUENCES: 6 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
CLASSIFICATION
                                           APPLICATION, NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
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60606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RMTWGKVTSLLIWVISLLVSLPQIIYGNV---FNLDKLICGY---HDEAISTVVLATQMT 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LPFWAYSAAKSWVFGVHFCKLIFAIYKMSFFSGMLLLLCISIDRYVAIVQAVSAHRHRAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KF-IRSTHWEYYAMTSFHYTIMVTEAIAYLRACLNPVLYAFVSLKFRKNFWKLVKDIGCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGFFLPLLTMIVCYSVIIKTLLHAGGFQKHRSLKIIFLVMAVFLLTQMPFN-----LM
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TELEFAX: (312) 474-0448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 358 amino acids
                                                                                                                                                                                                                                                                                             6300 Sears Tower,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                         Floppy disk
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36.9%; Pred. No. 1.6e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                  Novel Seven Transmembrane Receptors
                                             PCT/US93/11153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84;
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                                                                                                                                                                                                                                                                                                  South Wacker Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                           STREET: ULL
STREET: ULL
CITY: Chicago
CITY: Illinois
TTSA
                                                                                                                                                                                                                                                                   APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 31 TELECOMMUNICATION INFORMATION: TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                      TITLE OF INVENTION: NO NUMBER OF SEQUENCES: 6 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                           uence 15, Application US/08153848 ent No. 5759804
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 0
FILING DATE: 17-NOV-1992
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 APPLICATION NUMBER:
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                                                                                                                                                                                               6300 Sears Tower,
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Bicknell
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US/08/153,848
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Search completed: July 15, Job time : 28 secs

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Best Local :
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SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
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TELEX: 25-3856
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122; Conserv
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                                 PYLGVSHQWKSSEDNSKTFSASHNVEATSMF 340
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                                                                                                                                            IGFLVPLLAMSFCYLVIIRTLLQARNFERNKAIKVIIAVVVVFIVFQLPYNGVVLAQTVA 289
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Pred. No. 1.7e-43;
84; Mismatches 106
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